Ninety-three of the one hundred seventy-six black bean samples tested, showed positive results for internal blight contamination with the SEM-serology procedures the blight bacteria was detected in the States Anzoategui, Apure, Aragua, Carabobo, Monagas, Portuguesa, Sucre y Trujillo.

In the States Apure, Monagas, Sucre and Trujillo the blight bacteria has been found for the first time (1). The results indicated the necessity to do a similar study for the halo blight bacteria, (Pseudomonas phaseolicola), and to use an adecuate technique to detect the blight bacteria in the phytopathological analysis for bean seed, used in the Seed Certification Program in Venezuela.

Table 1: Detection of internal bacterial blight contamination in black bean seed lots of different seed classes in Venezuela*.

Class of seed	Samples number	Samples with blight	Percentage of blighted samples		
Genetic	4	4	100		
Registered	9	8	89		
Foundation	1	0	0		
Certified	45	14	31		
Harvested from farmer	64	40	63		
Harvested from experiments	53	27	51		

* Semiselective media and Ouchterlony Technique was used.

References:

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LINKAGE BETWEEN THE GENE CODING THE SMALL SUBUNIT OF RIBULOSE BISPHOSPHATE CARBOXYLASE AND THE GENE CODING MALIC ENZYME IN PHASEOLUS VULGARIS

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An F2 population derived from the cross 'Seafarer' x 'Pirate' was analyzed for segregation in 4 isozyme systems: adenylate kinase (AdK), shikimic dehydrogenase (SKDH), ribulose bisphosphate carboxylase (rubisco), and malic enzyme (ME). The F2 population was grown in the greenhouse at

Geneva, N.Y., and leaf tissue extracts were obtained as described in (1). Details of the electrophoretic techniques and assays involved were also described in reference 1. 'Seafarer' possessed the 'slow' allozyme for AdK and the fast allozyme for SKDH, rubisco and ME. 'Pirate' was homozygous for the alternative allele.

In each of the 4 isozyme systems assayed three distinct phenotypes were observed: 2 corresponding to those of the parents and a third identical to that seen in the F1 generation. The distribution of phenotypes within isozyme systems did not deviate significantly from that expected for two codominant alleles segregation at one locus (Table 1). The genes responsible for the polymorphism in AdK, SKDH, rubisco and ME were designated AdK, Skdh, rbcS and Me, respectively.

Table 1. Segregation in isozyme phenotype for ADK, SKDH, rubisco and ME in an F2 population derived form the cross 'Seafarer' x 'Pirate.'

		No. plant	s with designated p	henotype		
Isozyme	N	slow	heterozygous	fast	x ²	P
AdK SKDH Rubisco ME	53 61 60 62	17 14 16 16	23 28 26 34	13 19 18 12	1.5 1.2 1.2 1.1	>0.3 >0.5 >0.5 >0.5 >0.5

Analysis of joint segregation ratios between isozyme loci gave a significant deviation from random assortment only for the pair of loci rbcS and Me (Table 2). Obvious correlations between allozyme phenotype and segregation morphological characters such as seed shape and growth habit were not observed, preventing the association of the rbcS -- Me segment with any previously identified linkage group.

Table 2. Joint segregation data for rbcS and Me.

No. plants with designated phenotype 1										Recomb.	Std.		
N	S/S	S/H	S/F	H/S	H/H	H/F	F/S	F/H	F/F	x ²	fract.	error	
60	7	8	1	6	17	3	3	8	7	11.4	33	7.2	

¹Phenotype designations: S = homozygous for the slow allele; H =heterozygous; F = homozygous for the fast allele.

References

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